

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

10

Met Ala Arg Leu Phe Leu Phe Asp Gly Thr Ala Leu Ala Tyr Arg Ala
1 5 10 15

15

Tyr Tyr Ala Leu Asp Arg Ser Leu Ser Thr Ser Thr Gly Ile Pro Thr
20 25 30

20

Asn Ala Val Tyr Gly Val Ala Arg Met Leu Val Lys Phe Ile Lys Glu
35 40 45

25

His Ile Ile Pro Glu Lys Asp Tyr Ala Ala Val Ala Phe Asp Lys Lys
50 55 60

30

Ala Ala Thr Phe Arg His Lys Leu Leu Val Ser Asp Lys Ala Gln Arg
65 70 75 80

35

Pro Lys Thr Pro Ala Leu Leu Val Gln Gln Leu Pro Tyr Ile Lys Arg
85 90 95

40

Leu Ile Glu Ala Leu Gly Phe Lys Val Leu Glu Leu Glu Gly Tyr Glu
100 105 110

45

Ala Asp Asp Ile Ile Ala Thr Leu Ala Val Arg Ala Ala Arg Phe Leu
115 120 125

50

Met Arg Phe Ser Leu Ile Thr Gly Asp Lys Asp Met Leu Gln Leu Val
130 135 140

55

Asn Glu Lys Ile Lys Val Trp Arg Ile Val Lys Gly Ile Ser Asp Leu
145 150 155 160

60

Glu Leu Tyr Asp Ser Lys Lys Val Lys Glu Arg Tyr Gly Val Glu Pro
165 170 175

His Gln Ile Pro Asp Leu Leu Ala Leu Thr Gly Asp Asp Ile Asp Asn
180 185 190

Ile Pro Gly Val Thr Gly Ile Gly Glu Lys Thr Ala Val Gln Leu Leu
195 200 205

Gly Lys Tyr Arg Asn Leu Glu Tyr Ile Leu Glu His Ala Arg Glu Leu
210 215 220

Pro Gln Arg Val Arg Lys Ala Leu Leu Arg Asp Arg Glu Val Ala Ile
225 230 235 240

Leu Ser Lys Lys Leu Ala Thr Leu Val Thr Asn Ala Pro Val Glu Val
245 250 255

Asp Trp Glu Glu Met Lys Tyr Arg Gly Tyr Asp Lys Arg Lys Leu Leu
260 265 270

DOT 221 199TH 250

Pro Ile Leu Lys Glu Leu Glu Phe Ala Ser Ile Met Lys Glu Leu Gln
275 280 285

5 Leu Tyr Glu Glu Ala Glu Pro Thr Gly Tyr Glu Ile Val Lys Asp His
290 295 300

Lys Thr Phe Glu Asp Leu Ile Glu Lys Leu Lys Glu Val Pro Ser Phe
305 310 315 320

10 Ala Leu Asp Leu Glu Thr Ser Ser Leu Asp Pro Phe Asn Cys Glu Ile
325 330 335

Val Gly Ile Ser Val Ser Phe Lys Pro Lys Thr Ala Tyr Tyr Ile Pro
340 345 350

15 Leu His His Arg Asn Ala His Asn Leu Asp Glu Thr Leu Val Leu Ser
355 360 365

Lys Leu Lys Glu Ile Leu Glu Asp Pro Ser Ser Lys Ile Val Gly Gln
370 375 380

20 Asn Leu Lys Tyr Asp Tyr Lys Val Leu Met Val Lys Gly Ile Ser Pro
385 390 395 400

25 Val Tyr Pro His Phe Asp Thr Met Ile Ala Ala Tyr Leu Leu Glu Pro
405 410 415

Asn Glu Lys Lys Phe Asn Leu Glu Asp Leu Ser Leu Lys Phe Leu Gly
420 425 430

30 Tyr Lys Met Thr Ser Tyr Gln Glu Leu Met Ser Phe Ser Ser Pro Leu
435 440 445

35 Phe Gly Phe Ser Phe Ala Asp Val Pro Val Asp Lys Ala Ala Glu Tyr
450 455 460

Ser Cys Glu Asp Ala Asp Ile Thr Tyr Arg Leu Tyr Lys Ile Leu Ser
465 470 475 480

40 Met Lys Leu His Glu Ala Glu Leu Glu Asn Val Phe Tyr Arg Ile Glu
485 490 495

Met Pro Leu Val Asn Val Leu Ala Arg Met Glu Phe Asn Trp Val Tyr
500 505 510

45 Val Asp Thr Glu Phe Leu Lys Lys Leu Ser Glu Glu Tyr Gly Lys Lys
515 520 525

50 Leu Glu Glu Leu Ala Glu Lys Ile Tyr Gln Ile Ala Gly Glu Pro Phe
530 535 540

Asn Ile Asn Ser Pro Lys Gln Val Ser Asn Ile Leu Phe Glu Lys Leu
545 550 555 560

55 Gly Ile Lys Pro Arg Gly Lys Thr Thr Lys Thr Gly Asp Tyr Ser Thr
565 570 575

Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
580 585 590

60

001001-49-1160

Leu Ile Leu Glu Phe Arg Lys Ile Leu Lys Leu Lys Ser Thr Tyr Ile
 595 600 605
 5 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Phe His Ala
 610 620
 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
 625 630 635 640
 10 Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
 645 650 655
 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
 660 665 670
 15 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
 675 680 685
 20 Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
 690 695 700
 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
 705 710 715 720
 25 Met Arg Arg Val Gly Lys Met Val Asn Phe Ser Ile Ile Tyr Gly Val
 725 730 735
 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
 740 745 750
 30 Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
 755 760 765
 35 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
 770 775 780
 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
 785 790 795 800
 40 Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
 805 810 815
 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
 820 825 830
 45 Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
 835 840 845
 50 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
 850 855 860
 Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
 865 870 875 880
 55 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
 885 890

(2) INFORMATION FOR SEQ ID NO:2:

001001-1987-06

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 893 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

1	Met	Ala	Arg	Leu	Phe	Leu	Phe	Asp	Gly	Thr	Ala	Leu	Ala	Tyr	Arg	Ala
				5						10					15	
15	Tyr	Tyr	Ala	Leu	Asp	Arg	Ser	Leu	Ser	Thr	Ser	Thr	Gly	Ile	Pro	Thr
				20					25					30		
20	Asn	Ala	Val	Tyr	Gly	Val	Ala	Arg	Met	Leu	Val	Lys	Phe	Ile	Lys	Glu
			35					40					45			
25	His	Ile	Ile	Pro	Glu	Lys	Asp	Tyr	Ala	Ala	Val	Ala	Phe	Asp	Lys	Lys
		50					55					60				
30	Ala	Ala	Thr	Phe	Arg	His	Lys	Leu	Leu	Val	Ser	Asp	Lys	Ala	Gln	Arg
	65					70					75					80
35	Pro	Lys	Thr	Pro	Ala	Leu	Leu	Val	Gln	Gln	Leu	Pro	Tyr	Ile	Lys	Arg
					85					90					95	
40	Leu	Ile	Glu	Ala	Leu	Gly	Phe	Lys	Val	Leu	Glu	Leu	Glu	Gly	Tyr	Glu
				100					105					110		
45	Ala	Asp	Asp	Ile	Ile	Ala	Thr	Leu	Ala	Val	Arg	Ala	Ala	Arg	Phe	Leu
			115					120					125			
50	Met	Arg	Phe	Ser	Leu	Ile	Thr	Gly	Asp	Lys	Asp	Met	Leu	Gln	Leu	Val
		130					135					140				
55	Asn	Glu	Lys	Ile	Lys	Val	Trp	Arg	Ile	Val	Lys	Gly	Ile	Ser	Asp	Leu
	145					150					155					160
60	Glu	Leu	Tyr	Asp	Ser	Lys	Lys	Val	Lys	Glu	Arg	Tyr	Gly	Val	Glu	Pro
					165					170					175	
65	His	Gln	Ile	Pro	Asp	Leu	Leu	Ala	Leu	Thr	Gly	Asp	Asp	Ile	Asp	Asn
				180					185					190		
70	Ile	Pro	Gly	Val	Thr	Gly	Ile	Gly	Glu	Lys	Thr	Ala	Val	Gln	Leu	Leu
			195					200					205			
75	Gly	Lys	Tyr	Arg	Asn	Leu	Glu	Tyr	Ile	Leu	Glu	His	Ala	Arg	Glu	Leu
		210					215					220				
80	Pro	Gln	Arg	Val	Arg	Lys	Ala	Leu	Leu	Arg	Asp	Arg	Glu	Val	Ala	Ile
	225					230					235					240
85	Leu	Ser	Lys	Lys	Leu	Ala	Thr	Leu	Val	Thr	Asn	Ala	Pro	Val	Glu	Val
					245					250					255	
90	Asp	Trp	Glu	Glu	Met	Lys	Tyr	Arg	Gly	Tyr	Asp	Lys	Arg	Lys	Leu	Leu

00741661-1000

Arg Ile Glu Val Leu Glu Glu Ile Ala Asn Glu His Glu Ile Val Pro
580 585 590

5 Leu Ile Leu Glu Phe Arg Lys Ile Leu Lys Leu Lys Ser Thr Tyr Ile
595 600 605

10 Asp Thr Leu Pro Lys Leu Val Asn Pro Lys Thr Gly Arg Phe His Ala
610 615 620

15 Ser Phe His Gln Thr Gly Thr Ala Thr Gly Arg Leu Ser Ser Ser Asp
625 630 635 640

Pro Asn Leu Gln Asn Leu Pro Thr Lys Ser Glu Glu Gly Lys Glu Ile
645 650 655

20 Arg Lys Ala Ile Val Pro Gln Asp Pro Asp Trp Trp Ile Val Ser Ala
660 665 670

25 Asp Tyr Ser Gln Ile Glu Leu Arg Ile Leu Ala His Leu Ser Gly Asp
675 680 685

Glu Asn Leu Val Lys Ala Phe Glu Glu Gly Ile Asp Val His Thr Leu
690 695 700

30 Thr Ala Ser Arg Ile Tyr Asn Val Lys Pro Glu Glu Val Asn Glu Glu
705 710 715 720

Met Arg Arg Val Gly Lys Met Val Asn Tyr Ser Ile Ile Tyr Gly Val
725 730 735

35 Thr Pro Tyr Gly Leu Ser Val Arg Leu Gly Ile Pro Val Lys Glu Ala
740 745 750

Glu Lys Met Ile Ile Ser Tyr Phe Thr Leu Tyr Pro Lys Val Arg Ser
755 760 765

40 Tyr Ile Gln Gln Val Val Ala Glu Ala Lys Glu Lys Gly Tyr Val Arg
770 775 780

45 Thr Leu Phe Gly Arg Lys Arg Asp Ile Pro Gln Leu Met Ala Arg Asp
785 790 795 800

Lys Asn Thr Gln Ser Glu Gly Glu Arg Ile Ala Ile Asn Thr Pro Ile
805 810 815

50 Gln Gly Thr Ala Ala Asp Ile Ile Lys Leu Ala Met Ile Asp Ile Asp
820 825 830

Glu Glu Leu Arg Lys Arg Asn Met Lys Ser Arg Met Ile Ile Gln Val
835 840 845

55 His Asp Glu Leu Val Phe Glu Val Pro Asp Glu Glu Lys Glu Glu Leu
850 855 860

Val Asp Leu Val Lys Asn Lys Met Thr Asn Val Val Lys Leu Ser Val
865 870 875 880

60 Pro Leu Glu Val Asp Ile Ser Ile Gly Lys Ser Trp Ser
885 890

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